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1642
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In re Application of:

Boot et al.

Serial No.: 10/046,671

Filed: January 14, 2002

For: MOSAIC INFECTIOUS BURSAL
DISEASE VIRUS VACCINES

Examiner: To be assigned

Group Art Unit: 1642

Attorney Docket No.: 2183-5238US

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SEQUENCE STATEMENT

Commissioner for Patents
Washington, D.C. 20231

Sir:

I, Tawni L. Wilhelm, an attorney registered to practice before the United States Patent & Trademark Office and attorney of record for this application, state that:

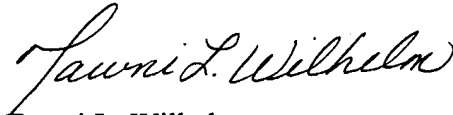
1. The enclosed paper copy of the SEQUENCE LISTING has been prepared to comply with the requirements of 37 C.F.R. §§ 1.822 and/or 1.823.

2. The enclosed paper copy of the SEQUENCE LISTING is believed to be the same as the paper copy of the SEQUENCE LISTING and the copy of the SEQUENCE LISTING in computer readable form (CRF) submitted in response to the Notice to File Missing Parts filed April 25, 2001.

Serial No.: 10/046,671

3. The SEQUENCE LISTING submitted herewith is believed to contain no "new matter" with regard to the referenced patent application.

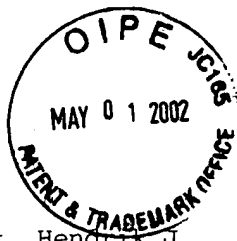
Respectfully submitted,

A handwritten signature in cursive script, reading "Tawni L. Wilhelm".

Tawni L. Wilhelm
Registration No. 47,456
Attorney for Applicants
TRASKBRITT, PC
P. O. Box 2550
Salt Lake City, Utah 84110-2550
Telephone: (801) 532-1922

Date: April 26, 2002

ACT/TLW/sw



SEQUENCE LISTING

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MAY 03 2002
TECH CENTER 1600/290

<110> Boot, Hendrik J.
Huurne ter, Anna A.H.M
Peeters, Bernardus P.H.

<120> Mosaic Infectious Bursal Disease Virus Vaccines

<130> 2183-5238US

<140> US 10/046,671

<141> 2002-01-14

<150> PCT/NL00/00493

<151> 2000-07-13

<150> EP 99202316.8

<151> 1999-07-14

<160> 87

<170> PatentIn Ver. 2.1

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 of IBDV

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<212> RNA
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<222> (1)..(10)
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5'-terminus of the A-segment coding strand of
IBDV

<400> 41
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<210> 42
<211> 4
<212> RNA
<213> Infectious bursal disease virus

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of the A-segment non-coding strand of IBDV

<400> 42
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<210> 43
<211> 8
<212> RNA
<213> Infectious bursal disease virus

<220>
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<400> 43
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8

<210> 44
<211> 9
<212> RNA
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<220>

<221> misc_RNA
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<400> 44
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<210> 45
 <211> 9
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 <213> Infectious bursal disease virus

<220>
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 <222> (1)..(9)
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 of the A-segment non-coding strand of IBDV

<400> 45
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9

<210> 46
 <211> 11
 <212> RNA
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<220>
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 <222> (1)..(11)
 <223> Complementary sequence of the 5'-terminus
 of the A-segment non-coding strand of IBDV

<400> 46
 cggguccccc c

11

<210> 47
 <211> 12
 <212> RNA
 <213> Infectious bursal disease virus

<220>
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 <222> (1)..(12)
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 of the A-segment non-coding strand of IBDV

<400> 47
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12

<210> 48

<211> 12
 <212> RNA
 <213> Infectious bursal disease virus

 <220>
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 of the A-segment non-coding strand of IBDV

<400> 48
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12

<210> 49
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 <212> RNA
 <213> Infectious bursal disease virus

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 IBDV

<400> 49
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9

<210> 50
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<400> 50
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<210> 51
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 <212> RNA
 <213> Infectious bursal disease virus

<220>
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<210> 56
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9

<210> 57
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<210> 58
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<223> Complementary sequence of the 5'-terminus
of the B-segment non-coding strand of IBDV

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11

<210> 59

<211> 11
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 IBDV

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<210> 61
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 <213> Infectious bursal disease virus

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 5123, 96-C6, 97-B4, 97-B5, 97-B6, Hungary, OKYM,
 TKSM and HK46

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 Thr Ile Thr Leu Phe Ser Ala Asn Ile Asp Ala Ile Thr Ser Leu Ser
 20 25 30
 Ile Gly Gly Glu Leu Val Phe Gln Thr Ser Val Gln Gly Leu Ile Leu
 35 40 45
 Gly Ala Thr Ile Tyr Leu Ile Gly Phe Asp Gly Thr Ala Val Ile Thr
 50 55 60

Arg Ala Val Ala Ala Asp Asn Gly Leu Thr Ala Gly Thr Asp Asn Leu
65 70 75 80

Met Pro Phe Asn Ile Val Ile Pro Thr Ser Glu Ile Thr Gln Pro Ile
85 90 95

Thr Ser Ile Lys Leu Glu Ile Val Thr Ser Lys Ser Gly Gly Gln Ala
100 105 110

Gly Asp Gln Met Ser Trp Ser
115

<210> 62
<211> 119
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<222> (1)..(119)
<223> Amino acid sequence of the hypervariable
region of VP2 of IBDV isolate 96-B4

<400> 62
Ala Ala Asp Asp Tyr Gln Phe Ser Ser Gln Tyr Gln Pro Gly Gly Val
1 5 10 15

Thr Ile Thr Leu Phe Ser Ala Asn Ile Asp Ala Ile Thr Ser Leu Ser
20 25 30

Val Gly Gly Glu Leu Val Phe Gln Thr Ser Val Gln Gly Leu Val Leu
35 40 45

Gly Ala Thr Ile Tyr Leu Ile Gly Phe Asp Gly Thr Thr Val Ile Thr
50 55 60

Arg Ala Val Ala Ala Asn Asn Gly Leu Thr Thr Gly Thr Asp Asn Leu
65 70 75 80

Leu Pro Phe Asn Ile Val Ile Pro Thr Asn Glu Ile Thr Gln Pro Ile
85 90 95

Thr Ser Ile Lys Leu Glu Ile Val Thr Ser Lys Ser Gly Gly Gln Ala
100 105 110

Gly Asp Gln Met Ser Trp Ser
115

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 <223> Amino acid sequence of the hypervariable
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<400> 63

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Thr	Ile	Thr	Leu	Phe	Ser	Ala	Asn	Ile	Asp	Ala	Ile	Thr	Ser	Leu	Ser
			20					25					30		
Ile	Gly	Gly	Glu	Leu	Val	Phe	Asn	Thr	Ser	Val	Gln	Gly	Leu	Ala	Leu
		35					40					45			
Asn	Ala	Thr	Ile	Tyr	Leu	Ile	Gly	Phe	Asp	Gly	Thr	Thr	Val	Ile	Thr
		50					55				60				
Arg	Ala	Val	Ala	Ser	Asp	Asn	Gly	Leu	Thr	Thr	Gly	Ile	Asp	Asn	Leu
65					70					75					80
Met	Pro	Phe	Asn	Ile	Val	Ile	Pro	Thr	Asn	Glu	Ile	Thr	Gln	Pro	Ile
				85					90					95	
Thr	Ser	Ile	Lys	Leu	Glu	Ile	Val	Thr	Ser	Lys	Ser	Gly	Gly	Gln	Ala
			100					105					110		
Gly	Asp	Gln	Met	Ser	Trp	Ser									
			115												

<210> 64
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 <222> (1)..(119)
 <223> Amino acid sequence of the hypervariable
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Thr	Ile	Thr	Leu	Phe	Ser	Ala	Asn	Ile	Asp	Ala	Ile	Thr	Ser	Leu	Ser
			20					25					30		
Val	Gly	Gly	Glu	Leu	Val	Phe	Gln	Thr	Ser	Val	Gln	Gly	Leu	Val	Leu
			35				40					45			
Gly	Ala	Thr	Ile	Tyr	Leu	Ile	Gly	Phe	Asp	Gly	Thr	Ala	Val	Ile	Thr

50 55 60
 Arg Ala Val Ala Ala Tyr Asn Gly Leu Thr Thr Gly Thr Asp Asn Leu
 65 70 75 80
 Leu Pro Phe Asn Ile Val Ile Pro Thr Asn Glu Ile Thr Gln Pro Ile
 85 90 95
 Thr Ser Ile Lys Leu Glu Ile Val Thr Ser Lys Ser Gly Gly Gln Ala
 100 105 110
 Gly Asp Gln Met Ser Trp Ser
 115

<210> 65
 <211> 119
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 <213> Infectious bursal disease virus

<220>
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 <223> Amino acid sequence of the hypervariable
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 20 25 30
 Ile Gly Gly Glu Leu Val Phe Gln Thr Ser Val Gln Gly Leu Ile Leu
 35 40 45
 Gly Ala Thr Ile Tyr Leu Ile Gly Phe Asp Gly Thr Ala Val Ile Thr
 50 55 60
 Arg Ala Val Ala Ala Asn Asn Gly Leu Thr Ala Gly Thr Asp Asn Leu
 65 70 75 80
 Met Pro Phe Asn Ile Val Ile Pro Thr Ser Glu Ile Thr Gln Pro Ile
 85 90 95
 Thr Ser Ile Lys Leu Glu Ile Val Thr Ser Lys Ser Gly Gly Gln Ala
 100 105 110
 Gly Asp Gln Met Ser Trp Ser
 115

<210> 66
 <211> 119
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<213> Infectious bursal disease virus

<220>

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<222> (1)..(119)

<223> Amino acid sequence of the hypervariable
region of VP2 of IBDV isolate Zoontjes

<400> 66

Ala Ala Asp Asp Tyr Gln Phe Ser Ser Gln Tyr Gln Ala Gly Gly Val
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Thr Ile Thr Leu Phe Ser Ala Asn Ile Asp Ala Ile Thr Ser Leu Ser
20 25 30

Ile Gly Gly Glu Leu Val Phe Gln Thr Ser Val Gln Gly Leu Ile Leu
35 40 45

Gly Ala Thr Ile Tyr Leu Ile Gly Phe Asp Gly Thr Ala Val Ile Thr
50 55 60

Arg Ala Val Ala Ala Asp Asn Gly Leu Thr Ala Gly Thr Asp Asn Leu
65 70 75 80

Met Pro Phe Asn Ile Val Ile Pro Thr Ser Glu Thr Thr Gln Pro Ile
85 90 95

Thr Ser Ile Lys Leu Val Ile Val Thr Ser Lys Ser Gly Gly Gln Ala
100 105 110

Gly Asp Gln Met Ser Trp Ser
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<211> 119

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<213> Infectious bursal disease virus

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<222> (1)..(119)

<223> Amino acid sequence of the hypervariable
region of VP2 of IBDV isolate OKYMT

<400> 67

Ala Ala Asp Asp Tyr Gln Phe Ser Ser Gln Tyr Gln Ala Gly Gly Val
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Thr Ile Thr Leu Phe Ser Ala Asn Ile Asp Ala Ile Thr Ser Leu Ser
20 25 30

Ile Gly Gly Glu Leu Val Phe Gln Thr Ser Val Gln Gly Leu Thr Leu
35 40 45

Gly Ala Thr Ile Tyr Leu Ile Gly Phe Asp Gly Thr Ala Val Ile Thr
 50 55 60
 Arg Ala Val Ala Ala Asn Asn Gly Leu Thr Thr Gly Thr Asp Asn Leu
 65 70 75 80
 Met Pro Phe Asn Ile Val Ile Pro Thr Ser Glu Ile Thr Gln Pro Ile
 85 90 95
 Thr Ser Ile Lys Leu Glu Ile Val Thr Phe Lys Ser Gly Gly Gln Ala
 100 105 110
 Gly Asp Gln Met Ser Trp Ser
 115

<210> 68
 <211> 119
 <212> PRT
 <213> Infectious bursal disease virus

<220>
 <221> DOMAIN
 <222> (1)..(119)
 <223> Amino acid sequence of the hypervariable
 region of VP2 of IBDV isolate TKSMT

<400> 68
 Ala Ala Asp Asp Tyr Gln Phe Ser Ser Gln Tyr Gln Ala Gly Gly Val
 1 5 10 15
 Thr Ile Thr Leu Phe Ser Ala Asn Ile Asp Ala Ile Thr Ser Leu Ser
 20 25 30
 Ile Gly Gly Glu Leu Val Phe His Thr Ser Val Gln Gly Leu Ile Leu
 35 40 45
 Asp Ala Thr Ile Tyr Leu Ile Gly Phe Asp Gly Thr Ala Val Thr Thr
 50 55 60
 Arg Ala Val Ala Ala Asn Asn Gly Leu Thr Thr Gly Thr Asp Asn Leu
 65 70 75 80
 Met Pro Phe Asn Ile Val Ile Pro Thr Ser Glu Ile Thr Gln Pro Ile
 85 90 95
 Thr Ser Ile Lys Leu Glu Ile Val Thr Ser Lys Ser Gly Gly Gln Ala
 100 105 110
 Gly Asp Gln Met Ser Trp Ser
 115

<210> 69
 <211> 119

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<212> PRT
<213> Infectious bursal disease virus

<220>
<221> DOMAIN
<222> (1)..(119)
<223> Amino acid sequence of the hypervariable
        region of VP2 of IBDV isolate HK46-NT

<400> 69
Ala Ala Asp Asp Tyr Gln Phe Ser Ser Gln Tyr Gln Ala Gly Gly Val
 1             5             10             15

Thr Ile Thr Leu Phe Ser Ala Asn Ile Asp Ala Ile Thr Ser Leu Ser
      20             25             30

Ile Gly Gly Glu Leu Val Phe Gln Thr Ser Val Gln Gly Leu Ile Leu
      35             40             45

Gly Ala Thr Ile Tyr Leu Ile Gly Phe Asp Gly Thr Ala Val Ile Thr
      50             55             60

Arg Ala Val Ala Ala Asn Asn Gly Leu Thr Thr Gly Thr Asp Asn Leu
      65             70             75             80

Met Pro Phe Asn Ile Val Ile Pro Thr Ser Glu Ile Thr Gln Pro Ile
      85             90             95

Thr Ser Ile Lys Leu Glu Ile Val Thr Ser Lys Ser Gly Gly Gln Ala
      100            105            110

Gly Asp Gln Met Ser Trp Ser
      115

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<210> 70
<211> 3260
<212> DNA
<213> Infectious bursal disease virus

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<220>
<221> misc_feature
<222> (1)..(3260)
<223> Consensus cDNA sequence of IBDV A-segment

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<400> 70
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gatcgacgcg atgacraacc tgcaagatca aaccaaacag attgttccgt tcatacggag 180
ccttctgatg ccaacaaccg gaccggcgtc cattccggac gacaccctrg agaagcacac 240
tctcagggtca gagacctcga cctacaattt gactgtgggg gacacagggg caggggcta 300
tgtctttttc cctggwttcc ctggctcaat tgtgggtgct cactacacac tgcagagcaa 360
tggaactac aagttcgatc agatgctcct gactgcccag aacctaccgg ccagytacaa 420
ctactgcagg ctagtgagtc ggagtctcac agtgagggtca agcactactyc ctggtggcgt 480
ttatgcacta aayggcacca taaacgccgt gaccttccaa ggaagcctga gtgaactgac 540

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agatgttagc	tacaatgggt	tgatgtctgc	aacagccaac	atcaacgaca	aaatygggaa	600
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tgtgagrcty	ggtgacccca	ttcccgwat	agggctygac	ccaaaaatgg	tagcmacatg	720
tgacagcagt	gacaggccca	gagctctacac	cataactgca	gccgatgatt	accaattctc	780
atcacagtac	caascagggtg	gggtaacaat	cacactgttc	tcagcyaya	tygatgccat	840
cacaagcctc	agcrtygggg	gagarctcgt	gtttcaaaca	agcgtccamg	gccttrtact	900
gggygcyacc	atctacctya	taggctttga	tgggacwgcg	gtaatcacca	grgctgtggc	960
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aacmarcag	ataaccagc	caatcacatc	catcaaactg	gagatagtga	cctccaaaag	1080
tggtggtcag	gcrggggatc	agatgtcrtg	gtcrgcaagw	gggagcctag	cagtgcagat	1140
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ggatccgttc	gcgggtcccc					3260

<210> 71

<211> 3260

<212> DNA

<213> Infectious bursal disease virus

<220>

<221> misc_feature

<222> (1)..(3260)

<223> cDNA sequence CEF94-A of IBV A-segment

<400> 71

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gtctcccgac accacccgcg caggtgtgga caccaattcg gacttacaac atcccaaatt 3240
ggatccgttc gcgggtcccc                                     3260

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<210> 72

<211> 3260

<212> DNA.

<213> Infectious bursal disease virus

<220>

<221> misc_feature

<222> (1)..(3260)

<223> cDNA sequence D6948-A of IBV A-segment

<400> 72

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gatcgagcgc atgacgaacc tgcaagatca aaccaacagc attgttccgt tcatacggag 180
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<210> 73
<211> 964
<212> DNA
<213> Infectious bursal disease virus

<220>
<221> misc_feature
<222> (1)..(964)
<223> cDNA sequence TY89-A of IBV A-segment

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<400> 73
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ccagaactcg aagacgctgt gcgtgcaatg gacgctgctg caaacgtcga cccattgttc 180
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caggccggaa gcaagtcgca gagggccaag tatggcacgg ctggctacgg agtggaggct 360
agaggcccca cgccagaaga ggcacagagg gagaaaagaca cacggatctc caagaagatg 420
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agggcagcca cgctgatcta cggggctcca ggacaggctg aaccaccca agccttcata 660
gacgaagtgc ccagggtcta tgaaatcaac catgggcgtg gtccaaacca ggagcagatg 720
aaggacctgc tcttgactgc gatggagatg aagcatcgca atcccaggcg ggctccacca 780
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<210> 74
<211> 2827
<212> DNA
<213> Infectious bursal disease virus

<220>

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<221> misc_feature
 <222> (1)..(2827)
 <223> Consensus cDNA sequence of IBDV B-segment

<400> 74

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rttttcaaya gtccac aggc gcgaag camg atmtcagcag cgttcggcat aaagcctacw 180
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ytkgccagcc ctagtcgwct ggcmaagttc ctcagrgara acggctacaa rrttytgacg 300
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ggcccc 2827

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<210> 75
 <211> 2827
 <212> DNA
 <213> Infectious bursal disease virus

<220>
 <221> misc_feature
 <222> (1)..(2827)
 <223> cDNA sequence CEF94-B of IBV B-segment

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 attttcaaca gtccacaggg gcgaagcacg atctcagcag cgttcggcat aaagcctact 180
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 cttgccagcc ctagtgcact ggcaaagttc ctcagagaga acggctacaa agttytgacg 300
 ccacggtctc tgcccgagaa tgaggagtat gagaccgacc aaatactccc agacttagca 360
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 caggagtact tcccaaagta ctaccaaca catcgcccta gcaaggagaa gcccaatgcg 480
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 gccaacgagg gcctaaagga tgaagtaacc ctcttgaccc aaaacataag ggacaaggcc 600
 tatggaagtg ggacctacat gggacaagca actcgacttg tggccatgaa ggaggtcgcc 660
 actggaagaa acccaaaca ggatcctcta aagcttggtt acacttttga gagcatcgcg 720
 cagctacttg acatcacact accggtaggc ccaccgggtg aggatgacaa gccctgggtg 780
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cttctcggag caggaacgag cagaccaatg gggatggagg ccccaacacg gtccaagaac 2700
gccgtgaaaa tggccaaacg gcggcaacgc caaaaggaga gccgccaaca gccatgatgg 2760
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ggcccccc 2827

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<210> 76
<211> 2827
<212> DNA
<213> Infectious bursal disease virus

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<220>
<221> misc_feature
<222> (1)..(2827)
<223> cDNA sequence D6948-B of IBV B-segment

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gttttcaata gtccacaggc gcgaagcaag atatcagcag cgttcggcat aaagcctaca 180
gctggacagg atgtggaaga actcctgatc cctaagggtc gggtgccacc tgaggatccc 240
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taccgccccg atatgcatt actcaagcag atgactact tgtttctcca ggttcccag 540
gccacagata accttaaaga tgaggtcacc ctactaacc aaaacattag agataaagcc 600
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<210> 77

<211> 1012

<212> PRT

<213> Infectious bursal disease virus

<220>

<221> DOMAIN

<222> (1)..(1012)

<223> Consensus sequence of IBV polyprotein, whereby the Xaa indicator may be any amino acid

<400> 77

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Met Thr Asn Leu Gln Asp Gln Thr Gln Gln Ile Val Pro Phe Ile Arg
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Ser Leu Leu Met Pro Thr Thr Gly Pro Ala Ser Ile Pro Asp Asp Thr
      20             25            30

```

```

Leu Glu Lys His Thr Leu Arg Ser Glu Thr Ser Thr Tyr Asn Leu Thr
    35             40            45

```

```

Val Gly Asp Thr Gly Ser Gly Leu Ile Val Phe Phe Pro Gly Phe Pro
    50             55            60

```

```

Gly Ser Ile Val Gly Ala His Tyr Thr Leu Gln Ser Asn Gly Asn Tyr
    65             70            75            80

```

```

Lys Phe Asp Gln Met Leu Leu Thr Ala Gln Asn Leu Pro Ala Ser Tyr
      85             90            95

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```

Asn Tyr Cys Arg Leu Val Ser Arg Ser Leu Thr Val Arg Ser Ser Thr
    100            105           110

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```

Leu Pro Gly Gly Val Tyr Ala Leu Asn Gly Thr Ile Asn Ala Val Thr
    115            120           125

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```

Phe Gln Gly Ser Leu Ser Glu Leu Thr Asp Val Ser Tyr Asn Gly Leu
    130            135           140

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```

Met Ser Ala Thr Ala Asn Ile Asn Asp Lys Ile Gly Asn Val Leu Val
    145            150           155           160

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Gly Glu Gly Val Thr Val Leu Ser Leu Pro Thr Ser Tyr Asp Leu Gly

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				165				170				175			
Tyr	Val	Arg	Leu	Gly	Asp	Pro	Ile	Pro	Ala	Ile	Gly	Leu	Asp	Pro	Lys
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Met	Val	Ala	Thr	Cys	Asp	Ser	Ser	Asp	Arg	Pro	Arg	Val	Tyr	Thr	Ile
		195					200					205			
Thr	Ala	Ala	Asp	Asp	Tyr	Gln	Phe	Ser	Ser	Gln	Tyr	Gln	Xaa	Gly	Gly
	210					215					220				
Val	Thr	Ile	Thr	Leu	Phe	Ser	Ala	Asn	Ile	Asp	Ala	Ile	Thr	Ser	Leu
225					230					235					240
Ser	Xaa	Gly	Gly	Glu	Leu	Val	Phe	Gln	Thr	Ser	Val	Xaa	Gly	Leu	Xaa
				245					250					255	
Leu	Gly	Ala	Thr	Ile	Tyr	Leu	Ile	Gly	Phe	Asp	Gly	Thr	Ala	Val	Ile
			260					265					270		
Thr	Arg	Ala	Val	Ala	Ala	Xaa	Asn	Gly	Leu	Thr	Xaa	Gly	Thr	Asp	Asn
		275					280					285			
Leu	Xaa	Pro	Phe	Asn	Xaa	Val	Ile	Pro	Thr	Xaa	Glu	Ile	Thr	Gln	Pro
	290					295					300				
Ile	Thr	Ser	Ile	Lys	Leu	Glu	Ile	Val	Thr	Ser	Lys	Ser	Gly	Gly	Gln
305					310					315					320
Ala	Gly	Asp	Gln	Met	Ser	Trp	Ser	Ala	Xaa	Gly	Ser	Leu	Ala	Val	Thr
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Ile	His	Gly	Gly	Asn	Tyr	Pro	Gly	Ala	Leu	Arg	Pro	Val	Thr	Leu	Val
			340					345					350		
Ala	Tyr	Glu	Arg	Val	Ala	Thr	Gly	Ser	Val	Val	Thr	Val	Ala	Gly	Val
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Ser	Asn	Phe	Glu	Leu	Ile	Pro	Asn	Pro	Glu	Leu	Ala	Lys	Asn	Leu	Val
	370					375					380				
Thr	Glu	Tyr	Gly	Arg	Phe	Asp	Pro	Gly	Ala	Met	Asn	Tyr	Thr	Lys	Leu
385					390					395					400
Ile	Leu	Ser	Glu	Arg	Asp	Arg	Leu	Gly	Ile	Lys	Thr	Val	Trp	Pro	Thr
				405					410					415	
Arg	Glu	Tyr	Thr	Asp	Phe	Arg	Glu	Tyr	Phe	Met	Glu	Val	Ala	Asp	Leu
			420					425					430		
Asn	Ser	Pro	Leu	Lys	Ile	Ala	Gly	Ala	Phe	Gly	Phe	Lys	Asp	Ile	Ile
		435					440					445			
Arg	Ala	Xaa	Arg	Arg	Ile	Ala	Val	Pro	Val	Val	Ser	Thr	Leu	Phe	Pro
	450					455					460				

Pro Ala Ala Pro Leu Ala His Ala Ile Gly Glu Gly Val Asp Tyr Leu
 465 470 475 480
 Leu Gly Asp Glu Ala Gln Ala Ala Ser Gly Thr Ala Arg Ala Ala Ser
 485 490 495
 Gly Lys Ala Arg Ala Ala Ser Gly Arg Ile Arg Gln Leu Thr Leu Ala
 500 505 510
 Ala Asp Lys Gly Tyr Glu Val Val Ala Asn Leu Phe Gln Val Pro Gln
 515 520 525
 Asn Pro Val Val Asp Gly Ile Leu Ala Ser Pro Gly Xaa Leu Arg Gly
 530 535 540
 Ala His Asn Leu Asp Cys Val Leu Arg Glu Gly Ala Thr Leu Phe Pro
 545 550 555 560
 Val Val Ile Thr Thr Val Glu Asp Ala Met Thr Pro Lys Ala Leu Asn
 565 570 575
 Ser Lys Met Phe Ala Val Ile Glu Gly Val Arg Glu Asp Leu Gln Pro
 580 585 590
 Pro Ser Gln Arg Gly Ser Phe Ile Arg Thr Leu Ser Gly His Arg Val
 595 600 605
 Tyr Gly Tyr Ala Pro Asp Gly Val Leu Pro Leu Glu Thr Gly Arg Asp
 610 615 620
 Tyr Thr Val Val Pro Ile Asp Asp Val Trp Asp Asp Ser Ile Met Leu
 625 630 635 640
 Ser Lys Asp Pro Ile Pro Pro Ile Val Gly Asn Ser Gly Asn Leu Ala
 645 650 655
 Ile Ala Tyr Met Asp Val Phe Arg Pro Lys Val Pro Ile His Val Ala
 660 665 670
 Met Thr Gly Ala Leu Asn Ala Xaa Gly Glu Ile Glu Xaa Val Ser Phe
 675 680 685
 Arg Ser Thr Lys Leu Ala Thr Ala His Arg Leu Gly Leu Lys Leu Ala
 690 695 700
 Gly Pro Gly Ala Phe Asp Val Asn Thr Gly Xaa Asn Trp Ala Thr Phe
 705 710 715 720
 Ile Lys Arg Phe Pro His Asn Pro Arg Asp Trp Asp Arg Leu Pro Tyr
 725 730 735
 Leu Asn Leu Pro Tyr Leu Pro Pro Asn Ala Gly Arg Gln Tyr His Leu
 740 745 750

Ala Met Ala Ala Ser Glu Phe Lys Glu Thr Pro Glu Leu Glu Ser Ala
 755 760 765
 Val Arg Ala Met Glu Ala Ala Ala Asn Val Asp Pro Leu Phe Gln Ser
 770 775 780
 Ala Leu Ser Val Phe Met Trp Leu Glu Glu Asn Gly Ile Val Thr Asp
 785 790 795 800
 Met Ala Asn Phe Ala Leu Ser Asp Pro Asn Ala His Arg Met Arg Asn
 805 810 815
 Phe Leu Ala Asn Ala Pro Gln Ala Gly Ser Lys Ser Gln Arg Ala Lys
 820 825 830
 Tyr Gly Thr Ala Gly Tyr Gly Val Glu Ala Arg Gly Pro Thr Pro Glu
 835 840 845
 Glu Ala Gln Arg Glu Lys Asp Thr Arg Ile Ser Lys Lys Met Glu Thr
 850 855 860
 Met Gly Ile Tyr Phe Ala Thr Pro Glu Trp Val Ala Leu Asn Gly His
 865 870 875 880
 Arg Gly Pro Ser Pro Gly Gln Leu Lys Tyr Trp Gln Asn Thr Arg Glu
 885 890 895
 Ile Pro Asp Pro Asn Glu Asp Tyr Leu Asp Tyr Val His Ala Glu Lys
 900 905 910
 Ser Arg Leu Ala Ser Glu Glu Gln Ile Leu Arg Ala Ala Thr Ser Ile
 915 920 925
 Tyr Gly Ala Pro Gly Gln Ala Glu Pro Pro Gln Ala Phe Ile Asp Glu
 930 935 940
 Val Ala Lys Val Tyr Glu Ile Asn His Gly Arg Gly Pro Asn Gln Glu
 945 950 955 960
 Gln Met Lys Asp Leu Leu Leu Thr Ala Met Glu Met Lys His Arg Asn
 965 970 975
 Pro Arg Arg Ala Pro Pro Lys Pro Lys Pro Lys Pro Asn Ala Pro Thr
 980 985 990
 Gln Arg Pro Pro Gly Arg Leu Gly Arg Trp Ile Arg Thr Val Ser Asp
 995 1000 1005
 Glu Asp Leu Glu
 1010

<210> 78
 <211> 1012
 <212> PRT

<213> Infectious bursal disease virus

<220>

<221> DOMAIN

<222> (1)..(1012)

<223> Sequence of IBDV polyprotein CEF94-PP

<400> 78

Met Thr Asn Leu Gln Asp Gln Thr Gln Gln Ile Val Pro Phe Ile Arg
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Ser Leu Leu Met Pro Thr Thr Gly Pro Ala Ser Ile Pro Asp Asp Thr
20 25 30

Leu Glu Lys His Thr Leu Arg Ser Glu Thr Ser Thr Tyr Asn Leu Thr
35 40 45

Val Gly Asp Thr Gly Ser Gly Leu Ile Val Phe Phe Pro Gly Phe Pro
50 55 60

Gly Ser Ile Val Gly Ala His Tyr Thr Leu Gln Ser Asn Gly Asn Tyr
65 70 75 80

Lys Phe Asp Gln Met Leu Leu Thr Ala Gln Asn Leu Pro Ala Ser Tyr
85 90 95

Asn Tyr Cys Arg Leu Val Ser Arg Ser Leu Thr Val Arg Ser Ser Thr
100 105 110

Leu Pro Gly Gly Val Tyr Ala Leu Asn Gly Thr Ile Asn Ala Val Thr
115 120 125

Phe Gln Gly Ser Leu Ser Glu Leu Thr Asp Val Ser Tyr Asn Gly Leu
130 135 140

Met Ser Ala Thr Ala Asn Ile Asn Asp Lys Ile Gly Asn Val Leu Val
145 150 155 160

Gly Glu Gly Val Thr Val Leu Ser Leu Pro Thr Ser Tyr Asp Leu Gly
165 170 175

Tyr Val Arg Leu Gly Asp Pro Ile Pro Ala Ile Gly Leu Asp Pro Lys
180 185 190

Met Val Ala Thr Cys Asp Ser Ser Asp Arg Pro Arg Val Tyr Thr Ile
195 200 205

Thr Ala Ala Asp Asp Tyr Gln Phe Ser Ser Gln Tyr Gln Pro Gly Gly
210 215 220

Val Thr Ile Thr Leu Phe Ser Ala Asn Ile Asp Ala Ile Thr Ser Leu
225 230 235 240

Ser Val Gly Gly Glu Leu Val Phe Gln Thr Ser Val His Gly Leu Val
245 250 255

Leu Gly Ala Thr Ile Tyr Leu Ile Gly Phe Asp Gly Thr Ala Val Ile
 260 265 270
 Thr Arg Ala Val Ala Ala Asn Asn Gly Leu Thr Thr Gly Thr Asp Asn
 275 280 285
 Leu Leu Pro Phe Asn Leu Val Ile Pro Thr Asn Glu Ile Thr Gln Pro
 290 295 300
 Ile Thr Ser Ile Lys Leu Glu Ile Val Thr Ser Lys Ser Gly Gly Gln
 305 310 315 320
 Ala Gly Asp Gln Met Ser Trp Ser Ala Arg Gly Ser Leu Ala Val Thr
 325 330 335
 Ile His Gly Gly Asn Tyr Pro Gly Ala Leu Arg Pro Val Thr Leu Val
 340 345 350
 Ala Tyr Glu Arg Val Ala Thr Gly Ser Val Val Thr Val Ala Gly Val
 355 360 365
 Ser Asn Phe Glu Leu Ile Pro Asn Pro Glu Leu Ala Lys Asn Leu Val
 370 375 380
 Thr Glu Tyr Gly Arg Phe Asp Pro Gly Ala Met Asn Tyr Thr Lys Leu
 385 390 395 400
 Ile Leu Ser Glu Arg Asp Arg Leu Gly Ile Lys Thr Val Trp Pro Thr
 405 410 415
 Arg Glu Tyr Thr Asp Phe Arg Glu Tyr Phe Met Glu Val Ala Asp Leu
 420 425 430
 Asn Ser Pro Leu Lys Ile Ala Gly Ala Phe Gly Phe Lys Asp Ile Ile
 435 440 445
 Arg Ala Ile Arg Arg Ile Ala Val Pro Val Val Ser Thr Leu Phe Pro
 450 455 460
 Pro Ala Ala Pro Leu Ala His Ala Ile Gly Glu Gly Val Asp Tyr Leu
 465 470 475 480
 Leu Gly Asp Glu Ala Gln Ala Ala Ser Gly Thr Ala Arg Ala Ala Ser
 485 490 495
 Gly Lys Ala Arg Ala Ala Ser Gly Arg Ile Arg Gln Leu Thr Leu Ala
 500 505 510
 Ala Asp Lys Gly Tyr Glu Val Val Ala Asn Leu Phe Gln Val Pro Gln
 515 520 525
 Asn Pro Val Val Asp Gly Ile Leu Ala Ser Pro Gly Val Leu Arg Gly
 530 535 540

Ala His Asn Leu Asp Cys Val Leu Arg Glu Gly Ala Thr Leu Phe Pro
 545 550 555 560
 Val Val Ile Thr Thr Val Glu Asp Ala Met Thr Pro Lys Ala Leu Asn
 565 570 575
 Ser Lys Met Phe Ala Val Ile Glu Gly Val Arg Glu Asp Leu Gln Pro
 580 585 590
 Pro Ser Gln Arg Gly Ser Phe Ile Arg Thr Leu Ser Gly His Arg Val
 595 600 605
 Tyr Gly Tyr Ala Pro Asp Gly Val Leu Pro Leu Glu Thr Gly Arg Asp
 610 615 620
 Tyr Thr Val Val Pro Ile Asp Asp Val Trp Asp Asp Ser Ile Met Leu
 625 630 635 640
 Ser Lys Asp Pro Ile Pro Pro Ile Val Gly Asn Ser Gly Asn Leu Ala
 645 650 655
 Ile Ala Tyr Met Asp Val Phe Arg Pro Lys Val Pro Ile His Val Ala
 660 665 670
 Met Thr Gly Ala Leu Asn Ala Cys Gly Glu Ile Glu Lys Val Ser Phe
 675 680 685
 Arg Ser Thr Lys Leu Ala Thr Ala His Arg Leu Gly Leu Lys Leu Ala
 690 695 700
 Gly Pro Gly Ala Phe Asp Val Asn Thr Gly Pro Asn Trp Ala Thr Phe
 705 710 715 720
 Ile Lys Arg Phe Pro His Asn Pro Arg Asp Trp Asp Arg Leu Pro Tyr
 725 730 735
 Leu Asn Leu Pro Tyr Leu Pro Pro Asn Ala Gly Arg Gln Tyr His Leu
 740 745 750
 Ala Met Ala Ala Ser Glu Phe Lys Glu Thr Pro Glu Leu Glu Ser Ala
 755 760 765
 Val Arg Ala Met Glu Ala Ala Ala Asn Val Asp Pro Leu Phe Gln Ser
 770 775 780
 Ala Leu Ser Val Phe Met Trp Leu Glu Glu Asn Gly Ile Val Thr Asp
 785 790 795 800
 Met Ala Asn Phe Ala Leu Ser Asp Pro Asn Ala His Arg Met Arg Asn
 805 810 815
 Phe Leu Ala Asn Ala Pro Gln Ala Gly Ser Lys Ser Gln Arg Ala Lys
 820 825 830
 Tyr Gly Thr Ala Gly Tyr Gly Val Glu Ala Arg Gly Pro Thr Pro Glu

835	840	845
Glu Ala Gln Arg Glu Lys Asp Thr Arg Ile Ser Lys Lys Met Glu Thr		
850	855	860
Met Gly Ile Tyr Phe Ala Thr Pro Glu Trp Val Ala Leu Asn Gly His		
865	870	875 880
Arg Gly Pro Ser Pro Gly Gln Leu Lys Tyr Trp Gln Asn Thr Arg Glu		
	885	890 895
Ile Pro Asp Pro Asn Glu Asp Tyr Leu Asp Tyr Val His Ala Glu Lys		
	900	905 910
Ser Arg Leu Ala Ser Glu Glu Gln Ile Leu Arg Ala Ala Thr Ser Ile		
	915	920 925
Tyr Gly Ala Pro Gly Gln Ala Glu Pro Pro Gln Ala Phe Ile Asp Glu		
	930	935 940
Val Ala Lys Val Tyr Glu Ile Asn His Gly Arg Gly Pro Asn Gln Glu		
945	950	955 960
Gln Met Lys Asp Leu Leu Leu Thr Ala Met Glu Met Lys His Arg Asn		
	965	970 975
Pro Arg Arg Ala Pro Pro Lys Pro Lys Pro Lys Pro Asn Ala Pro Thr		
	980	985 990
Gln Arg Pro Pro Gly Arg Leu Gly Arg Trp Ile Arg Thr Val Ser Asp		
	995	1000 1005
Glu Asp Leu Glu		
1010		

<210> 79
 <211> 1012
 <212> PRT
 <213> Infectious bursal disease virus

<220>
 <221> DOMAIN
 <222> (1)..(1012)
 <223> Sequence of IBDV polyprotein D6948-PP

<400> 79
Met Thr Asn Leu Gln Asp Gln Thr Gln Gln Ile Val Pro Phe Ile Arg
1 5 10 15
Ser Leu Leu Met Pro Thr Thr Gly Pro Ala Ser Ile Pro Asp Asp Thr
20 25 30
Leu Glu Lys His Thr Leu Arg Ser Glu Thr Ser Thr Tyr Asn Leu Thr
35 40 45

Ile His Gly Gly Asn Tyr Pro Gly Ala Leu Arg Pro Val Thr Leu Val
 340 345 350
 Ala Tyr Glu Arg Val Ala Thr Gly Ser Val Val Thr Val Ala Gly Val
 355 360 365
 Ser Asn Phe Glu Leu Ile Pro Asn Pro Glu Leu Ala Lys Asn Leu Val
 370 375 380
 Thr Glu Tyr Gly Arg Phe Asp Pro Gly Ala Met Asn Tyr Thr Lys Leu
 385 390 395 400
 Ile Leu Ser Glu Arg Asp Arg Leu Gly Ile Lys Thr Val Trp Pro Thr
 405 410 415
 Arg Glu Tyr Thr Asp Phe Arg Glu Tyr Phe Met Glu Val Ala Asp Leu
 420 425 430
 Asn Ser Pro Leu Lys Ile Ala Gly Ala Phe Gly Phe Lys Asp Ile Ile
 435 440 445
 Arg Ala Leu Arg Arg Ile Ala Val Pro Val Val Ser Thr Leu Phe Pro
 450 455 460
 Pro Ala Ala Pro Leu Ala His Ala Ile Gly Glu Gly Val Asp Tyr Leu
 465 470 475 480
 Leu Gly Asp Glu Ala Gln Ala Ala Ser Gly Thr Ala Arg Ala Ala Ser
 485 490 495
 Gly Lys Ala Arg Ala Ala Ser Gly Arg Ile Arg Gln Leu Thr Leu Ala
 500 505 510
 Ala Asp Lys Gly Tyr Glu Val Val Ala Asn Leu Phe Gln Val Pro Gln
 515 520 525
 Asn Pro Val Val Asp Gly Ile Leu Ala Ser Pro Gly Ile Leu Arg Gly
 530 535 540
 Ala His Asn Leu Asp Cys Val Leu Arg Glu Gly Ala Thr Leu Phe Pro
 545 550 555 560
 Val Val Ile Thr Thr Val Glu Asp Ala Met Thr Pro Lys Ala Leu Asn
 565 570 575
 Ser Lys Met Phe Ala Val Ile Glu Gly Val Arg Glu Asp Leu Gln Pro
 580 585 590
 Pro Ser Gln Arg Gly Ser Phe Ile Arg Thr Leu Ser Gly His Arg Val
 595 600 605
 Tyr Gly Tyr Ala Pro Asp Gly Val Leu Pro Leu Glu Thr Gly Arg Asp
 610 615 620
 Tyr Thr Val Val Pro Ile Asp Asp Val Trp Asp Asp Ser Ile Met Leu

625		630		635		640
Ser Lys Asp Pro	Ile Pro Pro Ile Val	Gly Asn Ser Gly Asn	Leu Ala			
	645	650	655			
Ile Ala Tyr Met	Asp Val Phe Arg Pro	Lys Val Pro Ile His	Val Ala			
	660	665	670			
Met Thr Gly Ala	Leu Asn Ala Tyr Gly	Glu Ile Glu Asn	Val Ser Phe			
	675	680	685			
Arg Ser Thr Lys	Leu Ala Thr Ala His	Arg Leu Gly Leu	Lys Leu Ala			
	690	695	700			
Gly Pro Gly Ala	Phe Asp Val Asn Thr	Gly Ser Asn Trp	Ala Thr Phe			
705	710	715	720			
Ile Lys Arg Phe	Pro His Asn Pro Arg	Asp Trp Asp Arg	Leu Pro Tyr			
	725	730	735			
Leu Asn Leu Pro	Tyr Leu Pro Pro Asn	Ala Gly Arg Gln	Tyr Asp Leu			
	740	745	750			
Ala Met Ala Ala	Ser Glu Phe Lys Glu	Thr Pro Glu Leu	Glu Ser Ala			
	755	760	765			
Val Arg Ala Met	Glu Ala Ala Ala Asn	Val Asp Pro Leu	Phe Gln Ser			
	770	775	780			
Ala Leu Ser Val	Phe Met Trp Leu Glu	Glu Asn Gly Ile	Val Thr Asp			
785	790	795	800			
Met Ala Asn Phe	Ala Leu Ser Asp Pro	Asn Ala His Arg	Met Arg Asn			
	805	810	815			
Phe Leu Ala Asn	Ala Pro Gln Ala Gly	Ser Lys Ser Gln	Arg Ala Lys			
	820	825	830			
Tyr Gly Thr Ala	Gly Tyr Gly Val Glu	Ala Arg Gly Pro	Thr Pro Glu			
	835	840	845			
Glu Ala Gln Arg	Glu Lys Asp Thr Arg	Ile Ser Lys Lys	Met Glu Thr			
	850	855	860			
Met Gly Ile Tyr	Phe Ala Thr Pro Glu	Trp Val Ala Leu	Asn Gly His			
865	870	875	880			
Arg Gly Pro Ser	Pro Gly Gln Leu Lys	Tyr Trp Gln Asn	Thr Arg Glu			
	885	890	895			
Ile Pro Asp Pro	Asn Glu Asp Tyr Leu	Asp Tyr Val His	Ala Glu Lys			
	900	905	910			
Ser Arg Leu Ala	Ser Glu Glu Gln Ile	Leu Arg Ala Ala	Thr Ser Ile			
	915	920	925			

Tyr Gly Ala Pro Gly Gln Ala Glu Pro Pro Gln Ala Phe Ile Asp Glu
 930 935 940
 Val Ala Lys Val Tyr Glu Ile Asn His Gly Arg Gly Pro Asn Gln Glu
 945 950 955 960
 Gln Met Lys Asp Leu Leu Leu Thr Ala Met Glu Met Lys His Arg Asn
 965 970 975
 Pro Arg Arg Ala Pro Pro Lys Pro Lys Pro Lys Pro Asn Ala Pro Thr
 980 985 990
 Gln Arg Pro Pro Gly Arg Leu Gly Arg Trp Ile Arg Ala Val Ser Asp
 995 1000 1005
 Glu Asp Leu Glu
 1010

<210> 80
 <211> 290
 <212> PRT
 <213> Infectious bursal disease virus

<220>
 <221> DOMAIN
 <222> (1)..(290)
 <223> Sequence of IBDV polyprotein TY89-PP

<400> 80
 Arg Phe Pro His Asn Pro Arg Asp Trp Asp Arg Leu Pro Tyr Leu Asn
 1 5 10 15
 Leu Pro Tyr Leu Pro Pro Thr Ala Gly Arg Gln Phe His Leu Ala Leu
 20 25 30
 Ala Ala Ser Glu Phe Lys Glu Thr Pro Glu Leu Glu Asp Ala Val Arg
 35 40 45
 Ala Met Asp Ala Ala Ala Asn Val Asp Pro Leu Phe Arg Ser Ala Leu
 50 55 60
 Gln Val Phe Met Trp Leu Glu Glu Asn Gly Ile Val Thr Asp Met Ala
 65 70 75 80
 Asn Phe Ala Leu Ser Asp Pro Asn Ala His Arg Met Lys Asn Phe Leu
 85 90 95
 Ala Asn Ala Pro Gln Ala Gly Ser Lys Ser Gln Arg Ala Lys Tyr Gly
 100 105 110
 Thr Ala Gly Tyr Gly Val Glu Ala Arg Gly Pro Thr Pro Glu Glu Ala
 115 120 125

Gln Arg Glu Lys Asp Thr Arg Ile Ser Lys Lys Met Glu Thr Met Gly
 130 135 140
 Ile Tyr Phe Ala Thr Pro Glu Trp Val Ala Leu Asn Gly His Arg Gly
 145 150 155 160
 Pro Ser Pro Gly Gln Leu Lys Tyr Trp Gln Asn Thr Arg Glu Ile Pro
 165 170 175
 Glu Pro Asn Glu Asp Tyr Pro Asp Tyr Val His Ala Glu Lys Ser Arg
 180 185 190
 Leu Ala Ser Glu Glu Gln Val Leu Arg Ala Ala Thr Ser Ile Tyr Gly
 195 200 205
 Ala Pro Gly Gln Ala Glu Pro Pro Gln Ala Phe Ile Asp Glu Val Ala
 210 215 220
 Arg Val Tyr Glu Ile Asn His Gly Arg Gly Pro Asn Gln Glu Gln Met
 225 230 235 240
 Lys Asp Leu Leu Leu Thr Ala Met Glu Met Lys His Arg Asn Pro Arg
 245 250 255
 Arg Ala Pro Pro Lys Pro Lys Pro Lys Pro Asn Ala Pro Ser Gln Arg
 260 265 270
 Pro Pro Gly Arg Leu Gly Arg Trp Ile Arg Thr Val Ser Asp Glu Asp
 275 280 285
 Leu Glu
 290

<210> 81
 <211> 881
 <212> PRT
 <213> Infectious bursal disease virus

<220>
 <221> DOMAIN
 <222> (1)..(881)
 <223> Consensus sequence of IBDV VP1, whereby the Xaa
 indicator may be any amino acid

<400> 81
 Met Ser Asp Xaa Phe Asn Ser Pro Gln Ala Arg Ser Xaa Ile Ser Ala
 1 5 10 15
 Ala Phe Gly Ile Lys Pro Thr Ala Gly Gln Asp Val Glu Glu Leu Leu
 20 25 30
 Ile Pro Lys Val Trp Val Pro Pro Glu Asp Pro Leu Ala Ser Pro Ser
 35 40 45

Arg Leu Ala Lys Phe Leu Arg Glu Asn Gly Tyr Lys Xaa Leu Gln Pro
 50 55 60
 Arg Ser Leu Pro Glu Asn Glu Glu Tyr Glu Thr Asp Gln Ile Leu Pro
 65 70 75 80
 Asp Leu Ala Trp Met Arg Gln Ile Glu Gly Ala Val Leu Lys Pro Thr
 85 90 95
 Leu Ser Leu Pro Ile Gly Asp Gln Glu Tyr Phe Pro Lys Tyr Tyr Pro
 100 105 110
 Thr His Arg Pro Ser Lys Glu Lys Pro Asn Ala Tyr Pro Pro Asp Ile
 115 120 125
 Ala Leu Leu Lys Gln Met Ile Tyr Leu Phe Leu Gln Val Pro Glu Ala
 130 135 140
 Xaa Xaa Xaa Leu Lys Asp Glu Val Thr Leu Leu Thr Gln Asn Ile Arg
 145 150 155 160
 Asp Lys Ala Tyr Gly Ser Gly Thr Tyr Met Gly Gln Ala Thr Arg Leu
 165 170 175
 Val Ala Met Lys Glu Val Ala Thr Gly Arg Asn Pro Asn Lys Asp Pro
 180 185 190
 Leu Lys Leu Gly Tyr Thr Phe Glu Ser Ile Ala Gln Leu Leu Asp Ile
 195 200 205
 Thr Leu Pro Val Gly Pro Pro Gly Glu Asp Asp Lys Pro Trp Val Pro
 210 215 220
 Leu Thr Arg Val Pro Ser Arg Met Leu Val Leu Thr Gly Asp Val Asp
 225 230 235 240
 Gly Xaa Phe Glu Val Glu Asp Tyr Leu Pro Lys Ile Asn Leu Lys Ser
 245 250 255
 Ser Ser Gly Leu Pro Tyr Val Gly Arg Thr Lys Gly Glu Thr Ile Gly
 260 265 270
 Glu Met Ile Ala Ile Ser Asn Gln Phe Leu Arg Glu Leu Ser Xaa Leu
 275 280 285
 Leu Lys Gln Gly Ala Gly Thr Lys Gly Ser Asn Lys Lys Lys Leu Leu
 290 295 300
 Ser Met Leu Ser Asp Tyr Trp Tyr Leu Ser Cys Gly Leu Leu Phe Pro
 305 310 315 320
 Lys Ala Glu Arg Tyr Asp Lys Ser Thr Trp Leu Thr Lys Thr Arg Asn
 325 330 335
 Ile Trp Ser Ala Pro Ser Pro Thr His Leu Met Ile Ser Met Ile Thr

340					345					350					
Trp	Pro	Val	Met	Ser	Asn	Ser	Pro	Asn	Asn	Val	Leu	Asn	Ile	Glu	Gly
		355					360					365			
Cys	Pro	Ser	Leu	Tyr	Lys	Phe	Asn	Pro	Phe	Arg	Gly	Gly	Leu	Asn	Arg
		370				375					380				
Ile	Val	Glu	Trp	Ile	Xaa	Ala	Pro	Xaa	Glu	Pro	Lys	Ala	Leu	Val	Tyr
385						390					395				400
Ala	Asp	Asn	Ile	Tyr	Ile	Val	His	Ser	Asn	Thr	Trp	Tyr	Ser	Ile	Asp
				405					410					415	
Leu	Glu	Lys	Gly	Glu	Ala	Asn	Cys	Thr	Arg	Gln	His	Met	Gln	Ala	Ala
			420					425					430		
Met	Tyr	Tyr	Ile	Leu	Thr	Arg	Gly	Trp	Ser	Asp	Asn	Gly	Asp	Pro	Met
			435				440					445			
Phe	Asn	Gln	Thr	Trp	Ala	Thr	Phe	Ala	Met	Asn	Ile	Ala	Pro	Ala	Leu
						455					460				
Val	Val	Asp	Ser	Ser	Cys	Leu	Ile	Met	Asn	Leu	Gln	Ile	Lys	Thr	Tyr
465						470					475				480
Gly	Gln	Gly	Ser	Gly	Asn	Ala	Ala	Thr	Phe	Ile	Asn	Asn	His	Leu	Leu
				485					490					495	
Ser	Thr	Leu	Val	Leu	Asp	Gln	Trp	Asn	Leu	Met	Xaa	Gln	Pro	Xaa	Pro
			500					505					510		
Asp	Ser	Glu	Glu	Phe	Lys	Ser	Ile	Glu	Asp	Lys	Leu	Gly	Ile	Asn	Phe
			515				520					525			
Lys	Ile	Glu	Arg	Ser	Ile	Asp	Asp	Ile	Arg	Gly	Lys	Leu	Arg	Gln	Leu
			530			535					540				
Val	Xaa	Leu	Ala	Gln	Pro	Gly	Tyr	Leu	Ser	Gly	Gly	Val	Glu	Pro	Glu
545						550					555				560
Gln	Xaa	Ser	Pro	Thr	Val	Glu	Leu	Asp	Leu	Leu	Gly	Trp	Ser	Ala	Thr
				565					570					575	
Tyr	Ser	Lys	Asp	Leu	Gly	Ile	Tyr	Val	Pro	Val	Leu	Asp	Lys	Glu	Arg
			580				585						590		
Leu	Phe	Cys	Ser	Ala	Ala	Tyr	Pro	Lys	Gly	Val	Glu	Asn	Lys	Ser	Leu
			595				600					605			
Lys	Ser	Lys	Val	Gly	Ile	Glu	Gln	Ala	Tyr	Lys	Val	Val	Arg	Tyr	Glu
			610			615					620				
Ala	Leu	Arg	Leu	Val	Gly	Gly	Trp	Asn	Tyr	Pro	Leu	Leu	Asn	Lys	Ala
625						630					635				640

Cys Lys Asn Asn Ala Xaa Ala Ala Arg Arg His Leu Glu Ala Lys Gly
 645 650 655
 Phe Pro Leu Asp Glu Phe Leu Ala Glu Trp Ser Glu Leu Ser Glu Phe
 660 665 670
 Gly Glu Ala Phe Glu Gly Phe Asn Ile Lys Leu Thr Val Thr Xaa Glu
 675 680 685
 Ser Leu Ala Glu Leu Asn Xaa Pro Val Pro Pro Lys Pro Pro Asn Val
 690 695 700
 Asn Arg Pro Val Asn Thr Gly Gly Leu Lys Ala Val Ser Asn Ala Leu
 705 710 715 720
 Lys Thr Gly Arg Tyr Arg Asn Glu Ala Gly Leu Ser Gly Leu Val Leu
 725 730 735
 Leu Ala Thr Ala Arg Ser Arg Leu Gln Asp Ala Val Lys Ala Lys Ala
 740 745 750
 Glu Ala Glu Lys Leu His Lys Ser Lys Pro Asp Asp Pro Asp Ala Asp
 755 760 765
 Trp Phe Glu Arg Ser Glu Thr Leu Ser Asp Leu Leu Glu Lys Ala Asp
 770 775 780
 Ile Ala Ser Lys Val Ala His Ser Ala Leu Val Glu Thr Ser Asp Ala
 785 790 795 800
 Leu Glu Ala Val Gln Ser Thr Ser Val Tyr Thr Pro Lys Tyr Pro Glu
 805 810 815
 Val Lys Asn Pro Gln Thr Ala Ser Asn Pro Val Val Gly Leu His Leu
 820 825 830
 Pro Ala Lys Arg Ala Thr Gly Val Gln Ala Ala Leu Leu Gly Ala Gly
 835 840 845
 Thr Ser Arg Pro Met Gly Met Glu Ala Pro Thr Arg Ser Lys Asn Ala
 850 855 860
 Val Lys Met Ala Lys Arg Arg Gln Arg Gln Lys Glu Ser Arg Gln Xaa
 865 870 875 880
 Xaa

<210> 82
 <211> 881
 <212> PRT
 <213> Infectious bursal disease virus
 <220>

<221> DOMAIN

<222> (1)..(881)

<223> Sequence of IBDV CEF94-VP1

<400> 82

Met	Ser	Asp	Ile	Phe	Asn	Ser	Pro	Gln	Ala	Arg	Ser	Thr	Ile	Ser	Ala
1				5				10					15		
Ala	Phe	Gly	Ile	Lys	Pro	Thr	Ala	Gly	Gln	Asp	Val	Glu	Glu	Leu	Leu
			20					25					30		
Ile	Pro	Lys	Val	Trp	Val	Pro	Pro	Glu	Asp	Pro	Leu	Ala	Ser	Pro	Ser
		35					40					45			
Arg	Leu	Ala	Lys	Phe	Leu	Arg	Glu	Asn	Gly	Tyr	Lys	Val	Leu	Gln	Pro
	50					55					60				
Arg	Ser	Leu	Pro	Glu	Asn	Glu	Glu	Tyr	Glu	Thr	Asp	Gln	Ile	Leu	Pro
	65				70					75					80
Asp	Leu	Ala	Trp	Met	Arg	Gln	Ile	Glu	Gly	Ala	Val	Leu	Lys	Pro	Thr
				85					90					95	
Leu	Ser	Leu	Pro	Ile	Gly	Asp	Gln	Glu	Tyr	Phe	Pro	Lys	Tyr	Tyr	Pro
		100						105					110		
Thr	His	Arg	Pro	Ser	Lys	Glu	Lys	Pro	Asn	Ala	Tyr	Pro	Pro	Asp	Ile
		115					120						125		
Ala	Leu	Leu	Lys	Gln	Met	Ile	Tyr	Leu	Phe	Leu	Gln	Val	Pro	Glu	Ala
	130					135					140				
Asn	Glu	Gly	Leu	Lys	Asp	Glu	Val	Thr	Leu	Leu	Thr	Gln	Asn	Ile	Arg
145					150					155					160
Asp	Lys	Ala	Tyr	Gly	Ser	Gly	Thr	Tyr	Met	Gly	Gln	Ala	Thr	Arg	Leu
				165					170					175	
Val	Ala	Met	Lys	Glu	Val	Ala	Thr	Gly	Arg	Asn	Pro	Asn	Lys	Asp	Pro
		180						185					190		
Leu	Lys	Leu	Gly	Tyr	Thr	Phe	Glu	Ser	Ile	Ala	Gln	Leu	Leu	Asp	Ile
		195					200					205			
Thr	Leu	Pro	Val	Gly	Pro	Pro	Gly	Glu	Asp	Asp	Lys	Pro	Trp	Val	Pro
	210					215						220			
Leu	Thr	Arg	Val	Pro	Ser	Arg	Met	Leu	Val	Leu	Thr	Gly	Asp	Val	Asp
225					230					235					240
Gly	Asp	Phe	Glu	Val	Glu	Asp	Tyr	Leu	Pro	Lys	Ile	Asn	Leu	Lys	Ser
			245						250					255	
Ser	Ser	Gly	Leu	Pro	Tyr	Val	Gly	Arg	Thr	Lys	Gly	Glu	Thr	Ile	Gly
			260					265					270		

Glu	Met	Ile	Ala	Ile	Ser	Asn	Gln	Phe	Leu	Arg	Glu	Leu	Ser	Thr	Leu	275	280	285	
Leu	Lys	Gln	Gly	Ala	Gly	Thr	Lys	Gly	Ser	Asn	Lys	Lys	Lys	Leu	Leu	290	295	300	
Ser	Met	Leu	Ser	Asp	Tyr	Trp	Tyr	Leu	Ser	Cys	Gly	Leu	Leu	Phe	Pro	305	310	315	320
Lys	Ala	Glu	Arg	Tyr	Asp	Lys	Ser	Thr	Trp	Leu	Thr	Lys	Thr	Arg	Asn	325	330	335	
Ile	Trp	Ser	Ala	Pro	Ser	Pro	Thr	His	Leu	Met	Ile	Ser	Met	Ile	Thr	340	345	350	
Trp	Pro	Val	Met	Ser	Asn	Ser	Pro	Asn	Asn	Val	Leu	Asn	Ile	Glu	Gly	355	360	365	
Cys	Pro	Ser	Leu	Tyr	Lys	Phe	Asn	Pro	Phe	Arg	Gly	Gly	Leu	Asn	Arg	370	375	380	
Ile	Val	Glu	Trp	Ile	Leu	Ala	Pro	Glu	Glu	Pro	Lys	Ala	Leu	Val	Tyr	385	390	395	400
Ala	Asp	Asn	Ile	Tyr	Ile	Val	His	Ser	Asn	Thr	Trp	Tyr	Ser	Ile	Asp	405	410	415	
Leu	Glu	Lys	Gly	Glu	Ala	Asn	Cys	Thr	Arg	Gln	His	Met	Gln	Ala	Ala	420	425	430	
Met	Tyr	Tyr	Ile	Leu	Thr	Arg	Gly	Trp	Ser	Asp	Asn	Gly	Asp	Pro	Met	435	440	445	
Phe	Asn	Gln	Thr	Trp	Ala	Thr	Phe	Ala	Met	Asn	Ile	Ala	Pro	Ala	Leu	450	455	460	
Val	Val	Asp	Ser	Ser	Cys	Leu	Ile	Met	Asn	Leu	Gln	Ile	Lys	Thr	Tyr	465	470	475	480
Gly	Gln	Gly	Ser	Gly	Asn	Ala	Ala	Thr	Phe	Ile	Asn	Asn	His	Leu	Leu	485	490	495	
Ser	Thr	Leu	Val	Leu	Asp	Gln	Trp	Asn	Leu	Met	Arg	Gln	Pro	Arg	Pro	500	505	510	
Asp	Ser	Glu	Glu	Phe	Lys	Ser	Ile	Glu	Asp	Lys	Leu	Gly	Ile	Asn	Phe	515	520	525	
Lys	Ile	Glu	Arg	Ser	Ile	Asp	Asp	Ile	Arg	Gly	Lys	Leu	Arg	Gln	Leu	530	535	540	
Val	Leu	Leu	Ala	Gln	Pro	Gly	Tyr	Leu	Ser	Gly	Gly	Val	Glu	Pro	Glu	545	550	555	560

Gln Ser Ser Pro Thr Val Glu Leu Asp Leu Leu Gly Trp Ser Ala Thr
 565 570 575
 Tyr Ser Lys Asp Leu Gly Ile Tyr Val Pro Val Leu Asp Lys Glu Arg
 580 585 590
 Leu Phe Cys Ser Ala Ala Tyr Pro Lys Gly Val Glu Asn Lys Ser Leu
 595 600 605
 Lys Ser Lys Val Gly Ile Glu Gln Ala Tyr Lys Val Val Arg Tyr Glu
 610 615 620
 Ala Leu Arg Leu Val Gly Gly Trp Asn Tyr Pro Leu Leu Asn Lys Ala
 625 630 635 640
 Cys Lys Asn Asn Ala Gly Ala Ala Arg Arg His Leu Glu Ala Lys Gly
 645 650 655
 Phe Pro Leu Asp Glu Phe Leu Ala Glu Trp Ser Glu Leu Ser Glu Phe
 660 665 670
 Gly Glu Ala Phe Glu Gly Phe Asn Ile Lys Leu Thr Val Thr Ser Glu
 675 680 685
 Ser Leu Ala Glu Leu Asn Lys Pro Val Pro Pro Lys Pro Pro Asn Val
 690 695 700
 Asn Arg Pro Val Asn Thr Gly Gly Leu Lys Ala Val Ser Asn Ala Leu
 705 710 715 720
 Lys Thr Gly Arg Tyr Arg Asn Glu Ala Gly Leu Ser Gly Leu Val Leu
 725 730 735
 Leu Ala Thr Ala Arg Ser Arg Leu Gln Asp Ala Val Lys Ala Lys Ala
 740 745 750
 Glu Ala Glu Lys Leu His Lys Ser Lys Pro Asp Asp Pro Asp Ala Asp
 755 760 765
 Trp Phe Glu Arg Ser Glu Thr Leu Ser Asp Leu Leu Glu Lys Ala Asp
 770 775 780
 Ile Ala Ser Lys Val Ala His Ser Ala Leu Val Glu Thr Ser Asp Ala
 785 790 795 800
 Leu Glu Ala Val Gln Ser Thr Ser Val Tyr Thr Pro Lys Tyr Pro Glu
 805 810 815
 Val Lys Asn Pro Gln Thr Ala Ser Asn Pro Val Val Gly Leu His Leu
 820 825 830
 Pro Ala Lys Arg Ala Thr Gly Val Gln Ala Ala Leu Leu Gly Ala Gly
 835 840 845
 Thr Ser Arg Pro Met Gly Met Glu Ala Pro Thr Arg Ser Lys Asn Ala

850 855 860
 Val Lys Met Ala Lys Arg Arg Gln Arg Gln Lys Glu Ser Arg Gln Gln
 865 870 875 880

 Pro

 <210> 83
 <211> 879
 <212> PRT
 <213> Infectious bursal disease virus

 <220>
 <221> DOMAIN
 <222> (1)..(879)
 <223> Sequence of IBV D6948-VP1

 <400> 83
 Met Ser Asp Val Phe Asn Ser Pro Gln Ala Arg Ser Lys Ile Ser Ala
 1 5 10 15

 Ala Phe Gly Ile Lys Pro Thr Ala Gly Gln Asp Val Glu Glu Leu Leu
 20 25 30

 Ile Pro Lys Val Trp Val Pro Pro Glu Asp Pro Leu Ala Ser Pro Ser
 35 40 45

 Arg Leu Ala Lys Phe Leu Arg Glu Asn Gly Tyr Lys Ile Leu Gln Pro
 50 55 60

 Arg Ser Leu Pro Glu Asn Glu Glu Tyr Glu Thr Asp Gln Ile Leu Pro
 65 70 75 80

 Asp Leu Ala Trp Met Arg Gln Ile Glu Gly Ala Val Leu Lys Pro Thr
 85 90 95

 Leu Ser Leu Pro Ile Gly Asp Gln Glu Tyr Phe Pro Lys Tyr Tyr Pro
 100 105 110

 Thr His Arg Pro Ser Lys Glu Lys Pro Asn Ala Tyr Pro Pro Asp Ile
 115 120 125

 Ala Leu Leu Lys Gln Met Ile Tyr Leu Phe Leu Gln Val Pro Glu Ala
 130 135 140

 Thr Asp Asn Leu Lys Asp Glu Val Thr Leu Leu Thr Gln Asn Ile Arg
 145 150 155 160

 Asp Lys Ala Tyr Gly Ser Gly Thr Tyr Met Gly Gln Ala Thr Arg Leu
 165 170 175

 Val Ala Met Lys Glu Val Ala Thr Gly Arg Asn Pro Asn Lys Asp Pro
 180 185 190

Leu Lys Leu Gly Tyr Thr Phe Glu Ser Ile Ala Gln Leu Leu Asp Ile
 195 200 205
 Thr Leu Pro Val Gly Pro Pro Gly Glu Asp Asp Lys Pro Trp Val Pro
 210 215 220
 Leu Thr Arg Val Pro Ser Arg Met Leu Val Leu Thr Gly Asp Val Asp
 225 230 235 240
 Gly Glu Phe Glu Val Glu Asp Tyr Leu Pro Lys Ile Asn Leu Lys Ser
 245 250 255
 Ser Ser Gly Leu Pro Tyr Val Gly Arg Thr Lys Gly Glu Thr Ile Gly
 260 265 270
 Glu Met Ile Ala Ile Ser Asn Gln Phe Leu Arg Glu Leu Ser Ala Leu
 275 280 285
 Leu Lys Gln Gly Ala Gly Thr Lys Gly Ser Asn Lys Lys Lys Leu Leu
 290 295 300
 Ser Met Leu Ser Asp Tyr Trp Tyr Leu Ser Cys Gly Leu Leu Phe Pro
 305 310 315 320
 Lys Ala Glu Arg Tyr Asp Lys Ser Thr Trp Leu Thr Lys Thr Arg Asn
 325 330 335
 Ile Trp Ser Ala Pro Ser Pro Thr His Leu Met Ile Ser Met Ile Thr
 340 345 350
 Trp Pro Val Met Ser Asn Ser Pro Asn Asn Val Leu Asn Ile Glu Gly
 355 360 365
 Cys Pro Ser Leu Tyr Lys Phe Asn Pro Phe Arg Gly Gly Leu Asn Arg
 370 375 380
 Ile Val Glu Trp Ile Met Ala Pro Asp Glu Pro Lys Ala Leu Val Tyr
 385 390 395 400
 Ala Asp Asn Ile Tyr Ile Val His Ser Asn Thr Trp Tyr Ser Ile Asp
 405 410 415
 Leu Glu Lys Gly Glu Ala Asn Cys Thr Arg Gln His Met Gln Ala Ala
 420 425 430
 Met Tyr Tyr Ile Leu Thr Arg Gly Trp Ser Asp Asn Gly Asp Pro Met
 435 440 445
 Phe Asn Gln Thr Trp Ala Thr Phe Ala Met Asn Ile Ala Pro Ala Leu
 450 455 460
 Val Val Asp Ser Ser Cys Leu Ile Met Asn Leu Gln Ile Lys Thr Tyr
 465 470 475 480
 Gly Gln Gly Ser Gly Asn Ala Ala Thr Phe Ile Asn Asn His Leu Leu

Ile Ala Ser Lys Val Ala His Ser Ala Leu Val Glu Thr Ser Asp Ala
 785 790 795 800
 Leu Glu Ala Val Gln Ser Thr Ser Val Tyr Thr Pro Lys Tyr Pro Glu
 805 810 815
 Val Lys Asn Pro Gln Thr Ala Ser Asn Pro Val Val Gly Leu His Leu
 820 825 830
 Pro Ala Lys Arg Ala Thr Gly Val Gln Ala Ala Leu Leu Gly Ala Gly
 835 840 845
 Thr Ser Arg Pro Met Gly Met Glu Ala Pro Thr Arg Ser Lys Asn Ala
 850 855 860
 Val Lys Met Ala Lys Arg Arg Gln Arg Gln Lys Glu Ser Arg Gln
 865 870 875

<210> 84
 <211> 145
 <212> PRT
 <213> Infectious bursal disease virus

<220>
 <221> DOMAIN
 <222> (1)..(145)
 <223> Consensus sequence of IBDV VP5, whereby the Xaa
 indicator may be any amino acid

<400> 84
 Met Val Ser Arg Asp Gln Thr Asn Asp Arg Ser Asp Asp Xaa Pro Ala
 1 5 10 15
 Arg Ser Asn Pro Thr Asp Cys Ser Val His Thr Glu Pro Ser Asp Ala
 20 25 30
 Asn Asn Arg Thr Gly Val His Ser Gly Arg His Pro Xaa Glu Ala His
 35 40 45
 Ser Gln Val Arg Asp Leu Asp Leu Gln Phe Asp Cys Gly Gly His Arg
 50 55 60
 Val Arg Ala Asn Cys Leu Phe Pro Trp Xaa Pro Trp Leu Asn Cys Gly
 65 70 75 80
 Cys Ser Leu His Thr Ala Glu Gln Trp Glu Leu Gln Val Arg Ser Asp
 85 90 95
 Ala Pro Asp Cys Pro Glu Pro Thr Gly Gln Leu Gln Leu Leu Gln Ala
 100 105 110
 Ser Glu Ser Glu Ser His Ser Glu Val Lys His Thr Xaa Trp Trp Arg

115		120		125
Leu Cys Thr Lys Xaa His His Lys Arg Arg Asp Leu Pro Arg Lys Pro				
130		135		140

Glu
145

<210> 85
 <211> 145
 <212> PRT
 <213> Infectious bursal disease virus

<220>
 <221> DOMAIN
 <222> (1)..(145)
 <223> Sequence of IBDV D6948-VP5

<400> 85
Met Val Ser Arg Asp Gln Thr Asn Asp Arg Ser Asp Asp Glu Pro Ala
1 5 10 15

Arg Ser Asn Pro Thr Asp Cys Ser Val His Thr Glu Pro Ser Asp Ala
20 25 30

Asn Asn Arg Thr Gly Val His Ser Gly Arg His Pro Arg Glu Ala His
35 40 45

Ser Gln Val Arg Asp Leu Asp Leu Gln Phe Asp Cys Gly Gly His Arg
50 55 60

Val Arg Ala Asn Cys Leu Phe Pro Trp Phe Pro Trp Leu Asn Cys Gly
65 70 75 80

Cys Ser Leu His Thr Ala Glu Gln Trp Glu Leu Gln Val Arg Ser Asp
85 90 95

Ala Pro Asp Cys Pro Glu Pro Thr Gly Gln Leu Gln Leu Leu Gln Ala
100 105 110

Ser Glu Ser Glu Ser His Ser Glu Val Lys His Thr Pro Trp Trp Arg
115 120 125

Leu Cys Thr Lys Trp His His Lys Arg Arg Asp Leu Pro Arg Lys Pro
130 135 140

Glu
145

<210> 86
 <211> 145
 <212> PRT
 <213> Infectious bursal disease virus

<220>
 <221> DOMAIN
 <222> (1)..(145)
 <223> Sequence of IBDV CEF94-VP5

 <400> 86
 Met Val Ser Arg Asp Gln Thr Asn Asp Arg Ser Asp Asp Lys Pro Ala
 1 5 10 15
 Arg Ser Asn Pro Thr Asp Cys Ser Val His Thr Glu Pro Ser Asp Ala
 20 25 30
 Asn Asn Arg Thr Gly Val His Ser Gly Arg His Pro Gly Glu Ala His
 35 40 45
 Ser Gln Val Arg Asp Leu Asp Leu Gln Phe Asp Cys Gly Gly His Arg
 50 55 60
 Val Arg Ala Asn Cys Leu Phe Pro Trp Ile Pro Trp Leu Asn Cys Gly
 65 70 75 80
 Cys Ser Leu His Thr Ala Glu Gln Trp Glu Leu Gln Val Arg Ser Asp
 85 90 95
 Ala Pro Asp Cys Pro Glu Pro Thr Gly Gln Leu Gln Leu Leu Gln Ala
 100 105 110
 Ser Glu Ser Glu Ser His Ser Glu Val Lys His Thr Ser Trp Trp Arg
 115 120 125
 Leu Cys Thr Lys Arg His His Lys Arg Arg Asp Leu Pro Arg Lys Pro
 130 135 140

 Glu
 145

<210> 87
 <211> 149
 <212> PRT
 <213> Infectious bursal disease virus

<220>
 <221> DOMAIN
 <222> (1)..(149)
 <223> Sequence of IBDV D6948-VP5

 <400> 87
 Met Leu Ser Leu Met Val Ser Arg Asp Gln Thr Asn Asp Arg Ser Asp
 1 5 10 15
 Asp Glu Pro Ala Arg Ser Asn Pro Thr Asp Cys Ser Val His Thr Glu
 20 25 30

Pro Ser Asp Ala Asn Asn Arg Thr Gly Val His Ser Gly Arg His Pro
 35 40 45
 Arg Glu Ala His Ser Gln Val Arg Asp Leu Asp Leu Gln Phe Asp Cys
 50 55 60
 Gly Gly His Arg Val Arg Ala Asn Cys Leu Phe Pro Trp Phe Pro Trp
 65 70 75 80
 Leu Asn Cys Gly Cys Ser Leu His Thr Ala Glu Gln Trp Glu Leu Gln
 85 90 95
 Val Arg Ser Asp Ala Pro Asp Cys Pro Glu Pro Thr Gly Gln Leu Gln
 100 105 110
 Leu Leu Gln Ala Ser Glu Ser Glu Ser His Ser Glu Val Lys His Thr
 115 120 125
 Pro Trp Trp Arg Leu Cys Thr Lys Trp His His Lys Arg Arg Asp Leu
 130 135 140
 Pro Arg Lys Pro Glu
 145